

AMENDMENT TO THE CLAIMS:

This listing of the claims will replace all prior versions, and listings, of the claims in the application.

1. (currently amended) An isolated polynucleotide comprising:
 - (a) a nucleotide sequence encoding a polypeptide required for proper root formation, wherein the polypeptide has an amino acid sequence of at least 70% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, ~~8, 30, or 38~~; or
 - (b) a complement of the nucleotide sequence, wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary.
2. (currently amended) The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 75% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, ~~8, 30, or 38~~;
3. (currently amended) The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 80% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, ~~8, 30, or 38~~;
4. (currently amended) The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 85% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, ~~8, 30, or 38~~;
5. (currently amended) The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 90% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, ~~8, 30, or 38~~;

6. (currently amended) The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 95% sequence identity, based on the Clustal V method of alignment, when compared to one of SEQ ID NO:6, ~~8, 30, or 38~~;

7. (currently amended) The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide has at least 99% sequence identity, based on the Clustal V method of alignment, when compared to SEQ ID NO: ~~6, 8, 30, or 38~~;

8. (currently amended) The polynucleotide of Claim 1, wherein the amino acid sequence of the polypeptide comprises one of SEQ ID NO:6, ~~8, 30, or 38~~;

9. (currently amended) The polynucleotide of Claim 1 wherein the nucleotide sequence comprises one of SEQ ID NO:5, ~~8, 30, or 38~~;

10. (currently amended) The isolated polynucleotide of Claim 1, wherein the nucleotide sequence comprises at least two motifs ~~selected from group~~ consisting of SEQ ID NOs:9[~~,11~~] and ~~10, 11, 12 and 13~~, wherein said motif is a substantially conserved subsequence.

11.(original) A functionally equivalent subfragment of the isolated polynucleotide of Claim 1, wherein said subfragment is useful in antisense inhibition or co-suppression of expression of a nucleic acid sequence encoding the polypeptide of Claim 1.

12. (canceled)

13. (original) A recombinant DNA construct comprising the isolated polynucleotide of Claim 1 or a functionally equivalent subfragment thereof, operably linked to at least one regulatory sequence.

14. (cancelled)

15. (original) A plant comprising in its genome the recombinant DNA construct of Claim 13.

16. (original) A seed obtained from the plant of Claim 15.

17. (original) The plant of Claim 15, wherein said plant is selected from the group consisting of rice, corn, sorghum, millet, rye, soybean, canola, wheat, barley, oat, beans, and nuts.

18. (original) Transformed plant tissue or plant cell comprising the recombinant DNA construct of Claim 13.

19. (original) A method of altering root structure during plant development, comprising:

- (a) transforming a plant with the recombinant DNA construct of Claim 13;
- (b) growing the transformed plant under conditions suitable for the expression of the recombinant DNA construct; and
- (c) selecting those transformed plants having altered root structure.

20-22 (cancelled)